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#6/10  
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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/715,927

DATE: 12/01/2000

TIME: 13:23:36

Input Set : A:\12421035-002 SEQ LISTING.TXT

Output Set: N:\CRF3\12012000\I715927.raw

**ENTERED**

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4 <110> APPLICANT: Zou, Leonard L.
5   Donovan, Adriana
7 <120> TITLE OF INVENTION: FERROPORIN1 NUCLEIC ACIDS AND PROTEINS
10 <130> FILE REFERENCE: 1242.1035-002
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/715,927
C--> 12 <141> CURRENT FILING DATE: 2000-11-17
12 <150> PRIOR APPLICATION NUMBER: US 60/133,382
13 <151> PRIOR FILING DATE: 1999-05-10
15 <150> PRIOR APPLICATION NUMBER: US 09/567,672
16 <151> PRIOR FILING DATE: 2000-05-09
18 <160> NUMBER OF SEQ ID NOS: 16
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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23 <211> LENGTH: 3773
24 <212> TYPE: DNA
25 <213> ORGANISM: Danio rerio
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (238)...(1926)
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33 ctgaaaaggt tatttctctc cgacttcagc tacagtgata gctaagtttg gagaggagaa 120
34 aagggagata ttctgtattt gcgcaggaat atatttgcag cgaggattta ctttgcccgga 180
35 gccttacaaa ggagttcaaa tcccggcgag aaaaaaaca tgcataaaaa acgcaca atg 240
36                                     Met
37                                     1
39 gac agc cct gca tca aag aaa cct cgc tgt gag agg ttc cgc gaa ttc 288
40 Asp Ser Pro Ala Ser Lys Lys Pro Arg Cys Glu Arg Phe Arg Glu Phe
41       5               10               15
43 ttc aag tct gca aaa ttc ctc att tac gtc gga cat gcc ctc tcg aca 336
44 Phe Lys Ser Ala Lys Phe Leu Ile Tyr Val Gly His Ala Leu Ser Thr
45       20               25               30
47 tgg ggg gat cgg atg tgg aat ttt gct gtg gct gtg ttt ctg gtg gag 384
48 Trp Gly Asp Arg Met Trp Asn Phe Ala Val Ala Val Phe Leu Val Glu
49       35               40               45
51 ctg tat gcc aat agt tta ctc ctg aca gcc gtg tat gga ctg gtg gtc 432
52 Leu Tyr Gly Asn Ser Leu Leu Leu Thr Ala Val Tyr Gly Leu Val Val
53       50               55               60               65
55 gcg ggc tcc gtg ctc tta ctg gcc gct att att ggt gac tgg gtt gac 480
56 Ala Gly Ser Val Leu Leu Leu Gly Ala Ile Ile Gly Asp Trp Val Asp
57       70               75               80
59 aaa aac ccc aga ttg aaa gtg gca cag acg tct ttg gtt gtc cag aac 528
60 Lys Asn Pro Arg Leu Lys Val Ala Gln Thr Ser Leu Val Val Gln Asn
61       85               90               95
63 agt gct gtc att ctc tgt ggt gcc ctt ttg atg gct gtt ttc cag ttc 576
64 Ser Ala Val Ile Leu Cys Gly Ala Leu Leu Met Ala Val Phe Gln Phe
65       100              105              110

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67 aaa caa cag ctt tct agc atg tat gat gga tgg ttg ctg aca aca tgc 624
68 Lys Gln Gln Leu Ser Ser Met Tyr Asp Gly Trp Leu Leu Thr Thr Cys
69 115 120 125
71 tac ata atg gtc atc tcc att gct aat atc gct aac ctg gcc agc aca 672
72 Tyr ile Met Val ile Ser ile Ala Asn ile Ala Asn Leu Ala Ser Thr
73 130 135 140 145
75 gct atg tcc atc acc atc caa aqa gac tgg gtt gtg gtt gtg gct gga 720
76 Ala Met Ser ile Thr ile Gln Arg Asp Trp Val Val Val Val Ala Gly
77 150 155 160
79 gat gat cgg agc aaa ttg gca gat atg aat gca act gtc aga ata att 768
80 Asp Asp Arg Ser Lys Leu Ala Asp Met Asn Ala Thr Val Arg ile ile
81 165 170 175
83 gac cag ttg acc aac att ctg gca ccg atg ctt gtg ggc cag atc atg 816
84 Asp Gln Leu Thr Asn ile Leu Ala Pro Met Leu Val Gly Gln ile Met
85 180 185 190
87 gca ttt ggc tca cac ttc att ggc tgt ggt ttt atc tgc ggc tgg aac 864
88 Ala Phe Gly Ser His Phe ile Gly Cys Gly Phe ile Ser Gly Trp Asn
89 195 200 205
91 ttg ttc tcc atg tgc ctg gag tat ttc ctg ctt tgg aaa gtt tat cag 912
92 Leu Phe Ser Met Cys Leu Glu Tyr Phe Leu Leu Trp Lys Val Tyr Gln
93 210 215 220 225
95 aaa act cca gcg ctt gcc ttt aag gca gga cag aag gat agc gat gac 960
96 Lys Thr Pro Ala Leu Ala Phe Lys Ala Gly Gln Lys Asp Ser Asp Asp
97 230 235 240
99 caa gag ctg aaa cac ctc aac ata caa aaa gaa att gga aac act gaa 1008
100 Gln Glu Leu Lys His Leu Asn ile Gln Lys Glu ile Gly Asn Thr Glu
101 245 250 255
103 agc ccg gtc gaa gcc tcc caa ctg atg act gaa agc tcc gag ccc aag 1056
104 Ser Pro Val Glu Ala Ser Gln Leu Met Thr Glu Ser Ser Glu Pro Lys
105 260 265 270
107 aag gac acc ggc tgc tgc tac caa atg gca gag ccc atc cgt acc ttt 1104
108 Lys Asp Thr Gly Cys Cys Tyr Gln Met Ala Glu Pro ile Arg Thr Phe
109 275 280 285
111 aaa gat ggc tgg gta gcc tac tac aat caa tcc atc ttc ttc gcc gcc 1152
112 Lys Asp Gly Trp Val Ala Tyr Tyr Asn Gln Ser ile Phe Phe Ala Gly
113 290 295 300 305
115 atg tct ctg gct ttc cta tac atg acc gtt ttg ggc ttc gac tgc atc 1200
116 Met Ser Leu Ala Phe Leu Tyr Met Thr Val Leu Gly Phe Asp Cys ile
117 310 315 320
119 acc aca ggc tat gca tac act cag ggc ctg aat ggc tct gtg etc agt 1248
120 Thr Thr Gly Tyr Ala Tyr Thr Gln Gly Leu Asn Gly Ser Val Leu Ser
121 325 330 335
123 etc etc atg gga gcc tca gct gta tct ggg atc tgt ggg aca gtg gcc 1296
124 Leu Leu Met Gly Ala Ser Ala Val Ser Gly ile Cys Gly Thr Val Ala
125 340 345 350
127 ttc acc tgg atc cga aag aag tgc ggc etc atc agg acg ggc ttc att 1344
128 Phe Thr Trp ile Arg Lys Lys Cys Gly Leu ile Arg Thr Gly Phe ile
129 355 360 365
131 gct gga gtc acc cag ctg tcc tgc etc acg ctg tgt gta gca tct gtc 1392

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132 Ala Gly Val Thr Gln Leu Ser Cys Leu Thr Leu Cys Val Ala Ser Val
133 370                               375                               380                               385
135 ttc gcc cct ggt agc cct ttc gat ctc agc gtc tcg ccc ttc aaa gag 1440
136 Phe Ala Pro Gly Ser Pro Phe Asp Leu Ser Val Ser Pro Phe Lys Glu
137                               390                               395                               400
139 gtc tta aga cat ctg ttt gga gac agc ggc tcg ctg cgt gag agt cct 1488
140 Val Leu Arg His Leu Phe Gly Asp Ser Gly Ser Leu Arg Glu Ser Pro
141                               405                               410                               415
143 aca ttc att cct aca act gaa ccc ccg att cag gcc aac gtc acc gtt 1536
144 Thr Phe Ile Pro Thr Thr Glu Pro Pro Ile Gln Ala Asn Val Thr Val
145                               420                               425                               430
147 ttt gag gaa gcc ccc cca gta gag tcc tac atg tct gtt ggg ctt ctc 1584
148 Phe Glu Glu Ala Pro Pro Val Glu Ser Tyr Met Ser Val Gly Leu Leu
149                               435                               440                               445
151 ttt gcc ggt gtt att gct gct aga gtt ggt ctt tgg tcc ttc gac ttg 1632
152 Phe Ala Gly Val Ile Ala Ala Arg Val Gly Leu Trp Ser Phe Asp Leu
153 450                               455                               460                               465
155 acc gtg acc caa ctg atc caa gag aat gtg att gag tcc gag aga gga 1680
156 Thr Val Thr Gln Leu Ile Gln Glu Asn Val Ile Glu Ser Glu Arg Gly
157                               470                               475                               480
159 gtc atc aat ggc gtc cag aac tcc atg aat tat ctt ctc gat ctc ctg 1728
160 Val Ile Asn Gly Val Gln Asn Ser Met Asn Tyr Leu Leu Asp Leu Leu
161                               485                               490                               495
163 cac ttc atc atg gtc atc ctt gca cca aat cct gaa gcc ttt ggt ctt 1776
164 His Phe Ile Met Val Ile Leu Ala Pro Asn Pro Glu Ala Phe Gly Leu
165                               500                               505                               510
167 ctt gta atc atc tcc gtt tcc ttc gtg gct atg gga cat atg atg tat 1824
168 Leu Val Ile Ile Ser Val Ser Phe Val Ala Met Gly His Met Met Tyr
169                               515                               520                               525
171 ttc agg ttt gct tat aaa agc ctt gga agc cga ctc ttc ctg ttc tgt 1872
172 Phe Arg Phe Ala Tyr Lys Ser Leu Gly Ser Arg Leu Phe Leu Phe Cys
173 530                               535                               540                               545
175 tca ccc gag cag aag cca gat ccc aac att ccc tca ctt cca aac tct 1920
176 Ser Pro Glu Gln Lys Pro Asp Pro Asn Ile Pro Ser Leu Pro Asn Ser
177                               550                               555                               560
179 gta tag ctttttaaaag agaccgtagg ccatttctac aagagcgtgg cttgctgtgt 1976
180 Val *
183 tcttttcagaa ccttgccagg atcccatctg ttttactaac atgcatgctt ttgctgcttg 2036
184 cagtgcctgtg cattgagtaa atatcctctg ccataggcta aaataacaaa gagaaggagc 2096
185 tcttcttagc atagcatact tcacttctca tatcatgttc aaggtgctgt aaaaatgcca 2156
186 tagaagcaac cgtaggagga aatatataca tggaaactac ggttctatca tgccttaatg 2216
187 acttttgtaa gagctccaaa gcaaaaatta gcatatttat tctactttta cgtattatat 2276
188 tgtttttttt ttccaacttt atggctgtag ttaaccttca gactggttat gacagttttg 2336
189 caatgtgctc taettatgat agtgtagttt tgtaatgttt gtcccttctt ccaagccttg 2396
190 gttaaagtct ctttaatagc tattaagagt gcgctagtta tacattcagg taagcctata 2456
191 taatgcctat atatttatat acacgtgtag tcagtattct ttatctcagc ttcggtgggtg 2516
192 ctacgttgtt tcaactcttt tggaaagcca tgcaggcggg ttatacatgt aaccaaagtg 2576
193 ggtttttttt ggcatacagt ggaagtgagg gaattgccgt ttttttatcg tgttaaacat 2636
194 tccatattat tattattacc ggtgtgatga tttcttgag atttaggcgc tyataggctc 2696

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195 cccatcgca gaaagatttt tagcgctagg tatttgtgct cctgtttgat ttgaaagtga 2756
196 ttltcgacac taattcttgt ttltatltgc aaagatttgt acacatgcac ttacatgat 2816
197 taatatacgt ttccattac gaaacaagcg caacaagccc tcaggtatta cgatatttgc 2876
198 acaatacaca aaacctgtcg ccgaagttca cggccaggca ggaatctga ttttttaca 2936
199 tgcaaattta ttcaaaatg ggattttcaa agtacattaa cctcaaaact catgattttt 2996
200 accttcctat ataagacacc acacctcata cgctaactta gattttctat aatacaaagt 3056
201 aagggttaca gactgttcta ttagctgaga tgaaagccac aatcatagaa gtactactaa 3116
202 cactctttta aaaccacagc tggctcgaca tagatatata gatatatata tatqaggtgt 3176
203 ttataatag ttgtgtaata ttgatgttg acaccagcgg gaatccacca tatgcacaga 3236
204 acagagaagg gattlattgag tccagtgtgt gaacggctgg ttgcaagcgc agctggttcc 3296
205 aaacacaggt gccaaagtcac acttgacttg ctaagttagc gttttcttta atgtgtgaga 3356
206 actacttcac gagggcccaa cgaacacact gtcagtcttt cattgtgtca gtctttctgt 3416
207 gaattgtgaag ccttattttac atctgtaaaa tttttttta tttcttatg ttgactagtt 3476
208 ttgtttcaat cgggtttatc ctcttttga aggcacaga ttcccccct ttagacaaga 3536
209 gaagtaaaaca catttgcaat aaattgtact tlcgacaccc agttgaatgt aacagaagaa 3596
210 cctagattat tctttatata agcatattga ttctgttcat gtttggtggc atatttgcaa 3656
211 taattgttgt tcacactcca tcgcagtggg aggattatag aactttagtc ttgtattgta 3716
212 tctcacttcg actgaaataa acagatttgt atctaaaaaa aaaaaaaa aaaaaaa 3773
214 <210> SEQ ID NO: 2
215 <211> LENGTH: 562
216 <212> TYPE: PRT
217 <213> ORGANISM: Danio rerio
219 <400> SEQUENCE: 2
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223 20 25 30
224 Thr Trp Gly Asp Arg Met Trp Asn Phe Ala Val Ala Val Phe Leu Val
225 35 40 45
226 Glu Leu Tyr Gly Asn Ser Leu Leu Leu Thr Ala Val Tyr Gly Leu Val
227 50 55 60
228 Val Ala Gly Ser Val Leu Leu Leu Gly Ala Ile Ile Gly Asp Trp Val
229 65 70 75 80
230 Asp Lys Asn Pro Arg Leu Lys Val Ala Gln Thr Ser Leu Val Val Gln
231 85 90 95
232 Asn Ser Ala Val Ile Leu Cys Gly Ala Leu Leu Met Ala Val Phe Gln
233 100 105 110
234 Phe Lys Gln Gln Leu Ser Ser Met Tyr Asp Gly Trp Leu Leu Thr Thr
235 115 120 125
236 Cys Tyr Ile Met Val Ile Ser Ile Ala Asn Ile Ala Asn Leu Ala Ser
237 130 135 140
238 Thr Ala Met Ser Ile Thr Ile Gln Arg Asp Trp Val Val Val Val Ala
239 145 150 155 160
240 Gly Asp Asp Arg Ser Lys Leu Ala Asp Met Asn Ala Thr Val Arg Ile
241 165 170 175
242 Ile Asp Gln Leu Thr Asn Ile Leu Ala Pro Met Leu Val Gly Gln Ile
243 180 185 190
244 Met Ala Phe Gly Ser His Phe Ile Gly Cys Gly Phe Ile Ser Gly Trp
245 195 200 205

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246 Asn Leu Phe Ser Met Cys Leu Glu Tyr Phe Leu Leu Trp Lys Val Tyr
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248 Gln Lys Thr Pro Ala Leu Ala Phe Lys Ala Gly Gln Lys Asp Ser Asp
249 225      230      235      240
250 Asp Gln Glu Leu Lys His Leu Asn Ile Gln Lys Glu Ile Gly Asn Thr
251      245      250      255
252 Glu Ser Pro Val Glu Ala Ser Gln Leu Met Thr Glu Ser Ser Glu Pro
253      260      265      270
254 Lys Lys Asp Thr Gly Cys Cys Tyr Gln Met Ala Glu Pro Ile Arg Thr
255      275      280      285
256 Phe Lys Asp Gly Trp Val Ala Tyr Tyr Asn Gln Ser Ile Phe Phe Ala
257      290      295      300
258 Gly Met Ser Leu Ala Phe Leu Tyr Met Thr Val Leu Gly Phe Asp Cys
259 305      310      315      320
260 Ile Thr Thr Gly Tyr Ala Tyr Thr Gln Gly Leu Asn Gly Ser Val Leu
261      325      330      335
262 Ser Leu Leu Met Gly Ala Ser Ala Val Ser Gly Ile Cys Gly Thr Val
263      340      345      350
264 Ala Phe Thr Trp Ile Arg Lys Lys Cys Gly Leu Ile Arg Thr Gly Phe
265      355      360      365
266 Ile Ala Gly Val Thr Gln Leu Ser Cys Leu Thr Leu Cys Val Ala Ser
267      370      375      380
268 Val Phe Ala Pro Gly Ser Pro Phe Asp Leu Ser Val Ser Pro Phe Lys
269 385      390      395      400
270 Glu Val Leu Arg His Leu Phe Gly Asp Ser Gly Ser Leu Arg Glu Ser
271      405      410      415
272 Pro Thr Phe Ile Pro Thr Thr Glu Pro Pro Ile Gln Ala Asn Val Thr
273      420      425      430
274 Val Phe Glu Glu Ala Pro Pro Val Glu Ser Tyr Met Ser Val Gly Leu
275      435      440      445
276 Leu Phe Ala Gly Val Ile Ala Ala Arg Val Gly Leu Trp Ser Phe Asp
277      450      455      460
278 Leu Thr Val Thr Gln Leu Ile Gln Glu Asn Val Ile Glu Ser Glu Arg
279 465      470      475      480
280 Gly Val Ile Asn Gly Val Gln Asn Ser Met Asn Tyr Leu Leu Asp Leu
281      485      490      495
282 Leu His Phe Ile Met Val Ile Leu Ala Pro Asn Pro Glu Ala Phe Gly
283      500      505      510
284 Leu Leu Val Ile Ile Ser Val Ser Phe Val Ala Met Gly His Met Met
285      515      520      525
286 Tyr Phe Arg Phe Ala Tyr Lys Ser Leu Gly Ser Arg Leu Phe Leu Phe
287      530      535      540
288 Cys Ser Pro Glu Gln Lys Pro Asp Pro Asn Ile Pro Ser Leu Pro Asn
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290 Ser Val
294 <210> SEQ ID NO: 3
295 <211> LENGTH: 2130
296 <212> TYPE: DNA
297 <213> ORGANISM: Mus musculus

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VERIFICATION SUMMARY                      DATE: 12/01/2000  
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date